

Significant association of TNF- α , but not other pro-inflammatory cytokines, single nucleotide polymorphisms with intervertebral disc degeneration in Iranian population

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Abstract

Objectives: As the important role of inflammation in pathophysiology of intervertebral disc degeneration and inconsistency regarding the role of pro-inflammatory cytokine genes SNPs, the current case-control study was designed to assess this in Iranian population. **Patients and Methods:** The genomic DNA of peripheral leukocytes of 76 patients and 140 healthy controls were investigated to sequence 9 SNPs of pro-inflammatory cytokine genes of interleukin 1 (IL-1), interleukin 6 (IL-6), and Tumor Necrosis Factor α (TNF- α) family. **Results:** ‘GA’ and ‘GG’ genotype of TNF- α –308 G/A SNP were significantly associated with IVDD. While ‘GA’ was 1.93 times more frequent in patients, the ‘GG’ genotype was more common among healthy subjects (OR = 0.51, P = 0.03). The ‘G’ allele of TNF- α –238 G/A was 2.51 times more common in IVDD patients while the ‘A’ genotype was more frequent in controls with odds ratio of 0.39 (P = 0.001). Interestingly, the homozygote ‘GG’ genotype was 2.98 times more prevalent in patients (P = 0.001) while the ‘GA’ heterozygote genotype was more common in healthy individuals (OR = 0.34). The other investigated SNPs were not significantly associated with disease in this study population. **Conclusion:** Polymorphisms of pro-inflammatory cytokine genes could take part in IVDD pathophysiology as the result of alteration in their expression levels or structures. The current study indicated significant roles of TNF- α –308 G/A and TNF- α –238 G/A SNPs with IVDD among Iranian patients. However, this study did not show any significant association between IVDD and either of SNPs of IL-1 and IL-6 genes